



#10

## SEQUENCE LISTING

&lt;110&gt; Liu, et al.

<120> Screens and Assays for Agents Useful in Controlling  
Parasitic Nematodes

&lt;130&gt; 2002630-0012

&lt;140&gt; 10/051,644

&lt;141&gt; 2002-01-18

&lt;160&gt; 8

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Amino Acid  
Sequence

&lt;400&gt; 1

Met Ala Val Leu Ala Val Val Leu Leu Leu Ala Cys Leu Glu Arg Ala  
1 5 10 15Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala  
20 25 30Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala  
35 40 45Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn  
50 55 60Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu  
65 70 75 80Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp  
85 90 95Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro  
100 105 110

Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val

	115		120		125												
Gly	Leu	Thr	Asp	Pro	Asp	Asn	Lys	Tyr	Thr	Asn	Ser	Ala	Met	Phe	Arg		
130						135					140						
Phe	Ala	Asn	Met	Ala	Asn	Gly	Lys	Ala	Ser	Ala	Phe	Gly	Cys	Ala	Tyr		
145					150					155					160		
Ala	Leu	Cys	Ala	Gly	Lys	Leu	Ser	Ile	Asn	Cys	Ile	Tyr	Asn	Lys	Ile		
				165					170					175			
Gly	Tyr	Met	Thr	Asn	Ala	Ile	Ile	Tyr	Glu	Lys	Gly	Asp	Ala	Cys	Thr		
			180					185					190				
Ser	Asp	Ala	Glu	Cys	Thr	Thr	Tyr	Ser	Asp	Ser	Gln	Cys	Lys	Asn	Gly		
	195						200					205					
Leu	Cys	Tyr	Lys	Ala	Pro	Gln	Ala	Pro	Val	Val	Glu	Thr	Phe	Thr	Met		
210						215					220						
Cys	Pro	Ser	Val	Thr	Asp	Gln	Ser	Asp	Gln	Ala	Arg	Gln	Asn	Phe	Leu		
225					230				235						240		
Asp	Thr	His	Asn	Lys	Leu	Arg	Thr	Ser	Leu	Ala	Lys	Gly	Leu	Glu	Ala		
				245					250					255			
Asp	Gly	Ile	Ala	Ala	Gly	Ala	Phe	Ala	Pro	Met	Ala	Lys	Gln	Met	Pro		
		260					265						270				
Lys	Leu	Val	Lys	Tyr	Ser	Cys	Thr	Val	Glu	Ala	Asn	Ala	Arg	Thr	Trp		
	275						280					285					
Ala	Lys	Gly	Cys	Leu	Tyr	Gln	His	Ser	Thr	Ser	Ala	Gln	Arg	Pro	Gly		
290						295					300						
Leu	Gly	Glu	Asn	Leu	Tyr	Met	Ile	Ser	Ile	Asn	Asn	Met	Pro	Lys	Ile		
305				310						315				320			
Gln	Thr	Ala	Glu	Asp	Ser	Ser	Lys	Ala	Trp	Trp	Ser	Glu	Leu	Lys	Asp		
				325					330					335			
Phe	Gly	Val	Gly	Ser	Asp	Asn	Ile	Leu	Thr	Gln	Ala	Val	Phe	Asp	Arg		
		340					345						350				
Gly	Val	Gly	His	Tyr	Thr	Gln	Met	Ala	Trp	Glu	Gly	Thr	Thr	Glu	Ile		
	355						360					365					
Gly	Cys	Phe	Val	Glu	Asn	Cys	Pro	Thr	Phe	Thr	Tyr	Ser	Val	Cys	Gln		

370                      375                      380  
 Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly  
 385                      390                      395                      400  
 Ser Pro Cys Thr Ala Asp Ala Asp Cys Pro Gly Thr Gln Thr Cys Ser  
                     405                      410                      415  
 Val Ala Glu Ala Leu Cys Val Ile Pro  
                     420                      425

<210> 2  
 <211> 1341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:cDNA Nucleotide  
 Sequence

<400> 2  
 atggcgggtat tagcagtggg actacttcta gcatgcctgg agagagcggg tgcacagacg 60  
 ttcggctgct ctaacaccaa gatcaatgac caggctcgta agatgttcta tgatgtctcac 120  
 aatgatgcaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180  
 ggtgaaaaga atgtttatga attgaattgg gattgcgaga tggaagcaaa agctcaggaa 240  
 tgggcagacg gatgtccag ctctttccag acatttgatc caacatgggg gcagaactac 300  
 gcgacgtaca tgggatcgat tgctgatccg ctccatacg cttccatggc tgtaaatggg 360  
 tgggtggtcgg aaattagaac cgtaggactt acggatcctg ataacaagta cactaacagt 420  
 gcaatgttcc gatttgctaa tatggcaaat ggtaaagctt cagcttttgg atgtgcatac 480  
 gcgttgtgcg caggaaaact atccatcaat tgcatttaca acaagatagg atacatgacc 540  
 aatgctatca tttatgaaaa aggagatgcc tgtaccagtg acgctgaatg caccacctac 600  
 tcagactcac aatgcaaaaa cggctcttgc tataaggcac ctcaagctcc agtcgttgag 660  
 actttcacia tgtgcccttc ggtaacggac cagtcggatc aggcgcgtca aaacttcttg 720  
 gacacccata acaaattgcg tacaagcctt gccaaaggac ttgaagctga tggaattgcc 780  
 gctggagcat ttgcaccaat ggccaagcaa atgccaaaac tggtaaaata cagctgcaca 840  
 gtgaagcaa acgccagaac atgggcaaaa ggatgccttt accagcattc aacaagcgca 900  
 cagagaccag gactcgggta aaatctttat atgatcagca ttaacaacat gcctaaaatt 960  
 caaaccgagg aggactcctc aaaggcttgg tggccgagt tgaaagactt cggagtcggg 1020  
 tctgacaaca ttctgaccca agcagttttt gatcgtggcg ttggacatta cacacaaatg 1080  
 gcatgggaag gaactactga aattggatgt tttgtggaga attgtccaac attcacttat 1140  
 tccgtatgcc aatatggtcc agcgggaaac tacatgaacc aactaatcta taccaagggc 1200  
 tcacatgca cagctgacgc cgattgcccc ggaaccaga catgcagtgt cgctgaagca 1260  
 ttatgtgtta tcccttagta aattttctat gcaactcttt gaaagtcata ataaatatgc 1320  
 aaaaattaaa aaaaaaaaaa a 1341

<210> 3

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid  
Sequence

<400> 3

Met Asn Val Val Leu Ser Ala Val Thr Leu Phe Leu Ile Phe Arg Tyr  
1 5 10 15

Ala Gln Thr Val Asn Ile Glu Gly Ser Gly Gly Asn Asp Glu Leu Leu  
20 25 30

Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu  
35 40 45

Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser  
50 55 60

Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu  
65 70 75 80

Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu  
85 90 95

Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu  
100 105 110

Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met  
115 120 125

Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr  
130 135 140

Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met  
145 150 155 160

Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys  
165 170 175

Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala  
180 185 190

Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp  
195 200 205

Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys  
 210 215 220

Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys  
 225 230 235 240

Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu  
 245 250 255

Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys  
 260 265 270

Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln  
 275 280 285

His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly  
 290 295 300

Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu  
 305 310 315 320

Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys  
 325 330 335

Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn  
 340 345 350

Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His  
 355 360 365

Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro  
 370 375 380

Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala  
 385 390 395 400

Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly  
 405 410 415

Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr  
 420 425 430

Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp  
 435 440 445

Pro Cys Glu Val Asp Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys  
 450 455 460

Thr Thr Ser Leu Cys Val Ile Ser Lys  
465 470

<210> 4  
<211> 1422  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:cDNA Nucleotide  
Sequence

<400> 4  
atgaacgtgg tcctttccgc tgtcactcctt tttcttattt ttcgatatgc gcagactgtg 60  
aatatagaag gcagtgaggg aaatgatgag cttcttgagc agaacgtgtg gaacgatgta 120  
gacgacaagg ttgtagaagc acttggtggt cttgatgatg aactgctaac cgaacatgtg 180  
tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa 240  
ttacgaagat cattggcitt cggaaagcaa agaaacaaga gaggtctcat gaacggtgcg 300  
agaaatatgt ataaactgga ttgggattgt gaactggcat cacttgcagc caattggtca 360  
acctcctgcc ctcagcactt tatgccgcaa tcggtacttg gctccaacgc tcagcttttt 420  
aagcgtttct atttttattt tgatgggcac gactctactg tacatatgcg aaacgcgatg 480  
aagtattggt ggcagcaagg tgaagaaaaa ggcaatgagg atcagaaaaa tagattctat 540  
gccagacgaa attatttttg atgggcaaac atggcaaaag gaaaaacata tcgagttgga 600  
tgctcgata ttatgtgcgg cgacggtgaa tctgcacttt tcaattgtct ttataacgaa 660  
aaagcccaat gcgaaaaaga aatgatattac gaaaatggaa aaccctgctg tgaggataaa 720  
gactgtttca catatccagg atcaaaatgt ttagtacctg aaggattatg tcaagcacct 780  
tctatggtaa aggatgatgg aggaagtttc caatgtgata actcccttgt gtcagatgtc 840  
acccgcaatt tcacttttga gcaacacaat ttttatagat ctctgtcttg aaaaggtttt 900  
gaatggaatg gagaaacaaa cacttcccag ccaaaggcta gtcaaataat caaaatggag 960  
tatgactgca tggttgaacg gtttgacaaa aactgggcaa ataattgctg ttttgcacac 1020  
tcggcacatt acgaaagacc gaatcagggg cagaatctct acatgagttc tttctcaaac 1080  
cctgaccta gaagccttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140  
ttcggctact caattgataa cgttctgaca cccgaattgt gggatttgaa agggaaagcg 1200  
ataggacatt aactcagat ggccctggat cgtacttacc gtcttggttg tggaatcgca 1260  
aactgtccga agatgtcgta cgtggtttgt cactatgggc cagcaggcaa cagaaagaac 1320  
aataaaaatct atgaaatcgg ggatccttgc gaagtcgatg atgattgccc gattggaaca 1380  
gattgtgaaa agacaacttc tttatgtgtg atctcaaaat aa 1422

<210> 5  
<211> 218  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and Selected Other

Nematode VA Proteins.

<400> 5

Met Phe Ser Pro Val Ile Val Ser Val Ile Phe Thr Ile Ala Phe Cys  
1 5 10 15

Asp Ala Ser Pro Ala Arg Asp Gly Phe Gly Cys Ser Asn Ser Gly Ile  
20 25 30

Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg  
35 40 45

Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn  
50 55 60

Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln  
65 70 75 80

Gln Leu Gln Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile  
85 90 95

Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe  
100 105 110

Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser  
115 120 125

Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly  
130 135 140

Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu  
145 150 155 160

Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile  
165 170 175

Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly  
180 185 190

Gln Ala Cys Lys Thr Gly Ala Asp Cys Ser Thr Tyr Lys Asn Ser Gly  
195 200 205

Cys Glu Asp Gly Leu Cys Thr Lys Gly Pro  
210 215

<210> 6

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and selected other  
nematode VA Proteins.

<400> 6

Asp Val Pro Glu Thr Asn Gln Gln Cys Pro Ser Asn Thr Gly Met Thr  
1 5 10 15

Asp Ser Val Arg Asp Thr Phe Leu Val His Asn Glu Phe Arg Ser Ser  
20 25 30

Val Ala Arg Gly Leu Glu Pro Asp Ala Leu Gly Gly Asn Ala Pro Lys  
35 40 45

Ala Ala Lys Met Leu Lys Met Val Tyr Asp Cys Glu Val Glu Ala Ser  
50 55 60

Ala Ile Arg His Gly Asn Lys Cys Val Tyr Gln His Ser His Gly Glu  
65 70 75 80

Asp Arg Pro Gly Leu Gly Glu Asn Ile Tyr Lys Thr Ser Val Leu Lys  
85 90 95

Phe Asp Lys Asn Lys Ala Ala Lys Gln Ala Ser Gln Leu Trp Trp Asn  
100 105 110

Glu Leu Lys Glu Phe Gly Val Gly Pro Ser Asn Val Leu Thr Thr Ala  
115 120 125

Leu Trp Asn Arg Pro Gly Met Gln Ile Gly His Tyr Thr Gln Met Ala  
130 135 140

Trp Asp Thr Thr Tyr Lys Leu Gly Cys Ala Val Val Phe Cys Asn Asp  
145 150 155 160

Phe Thr Phe Gly Val Cys Gln Tyr Gly Pro Gly Gly Asn Tyr Met Gly  
165 170 175

His Val Ile Tyr Thr Met Gly Gln Pro Cys Ser Gln Cys Ser Pro Gly  
180 185 190

Ala Thr Cys Ser Val Thr Glu Gly Leu Cys Ser Ala Pro  
195 200 205

<210> 7  
 <211> 207  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Clustal W  
 Alignment of VAP-1, VAP-2, and selected other  
 nematode VA proteins.

<400> 7  
 Met Asn Tyr Leu Leu Leu Val Val Ala Leu Ala Val Gly Cys Ser Ala  
 1 5 10 15  
 Asp Phe Gly Ser Ser Gly Gln Asn Gly Ile Ile Asn Ala His Asn Thr  
 20 25 30  
 Leu Arg Ser Lys Ile Ala Lys Gly Thr Tyr Val Ala Lys Gly Thr Gln  
 35 40 45  
 Lys Ser Pro Gly Thr Asn Leu Leu Lys Met Lys Trp Asp Ser Ala Val  
 50 55 60  
 Ala Ala Ser Ala Gln Asn Tyr Ala Asn Gly Cys Pro Thr Gly His Ser  
 65 70 75 80  
 Gly Asp Ala Gly Leu Gly Glu Asn Leu Tyr Trp Tyr Trp Thr Ser Gly  
 85 90 95  
 Ser Leu Gly Asp Leu Asn Gln Tyr Gly Ser Ala Ala Ser Ala Ser Trp  
 100 105 110  
 Glu Lys Glu Phe Gln Asp Tyr Gly Trp Lys Ser Asn Leu Met Thr Ile  
 115 120 125  
 Asp Leu Phe Asn Thr Gly Ile Gly His Ala Thr Gln Met Ala Trp Ala  
 130 135 140  
 Lys Ser Asn Leu Ile Gly Cys Gly Val Lys Asp Cys Gly Arg Asp Ser  
 145 150 155 160  
 Asn Gly Leu Asn Lys Val Thr Val Val Cys Gln Tyr Lys Pro Gln Gly  
 165 170 175  
 Asn Phe Ile Asn Gln Tyr Ile Tyr Val Ser Gly Ala Thr Cys Ser Gly  
 180 185 190

Cys Pro Ser Gly Thr Ser Cys Glu Thr Ser Thr Gly Leu Cys Val  
 195 200 205

<210> 8

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W  
 Alignment of VAP-1, VAP-2, and selected other  
 nematode VA proteins.

<400> 8

Met Ser Asn Lys Leu Ile Ile Ser Ile Leu Ile Leu Thr Ile Ile Tyr  
 1 5 10 15

Thr Val Val Asn Ser Leu Thr Val Pro Glu Gln Asn Ala Val Val Asp  
 20 25 30

Cys Ile Asn Lys Tyr Arg Ser Gln Leu Ala Asn Gly Lys Thr Lys Asn  
 35 40 45

Lys Asn Gly Gly Asn Phe Pro Ser Gly Lys Asp Ile Leu Glu Val Ser  
 50 55 60

Tyr Ser Lys Asp Leu Glu Lys Ser Ala Gln Arg Trp Ala Asn Lys Cys  
 65 70 75 80

Ile Phe Asp His Asn Gly Thr Asp Leu Tyr Ser Gly Gly Lys Phe Tyr  
 85 90 95

Gly Glu Asn Leu Tyr Leu Asp Gly Asp Phe Glu His Lys Asn Ile Thr  
 100 105 110

Gln Leu Met Ile Asp Ala Cys Asn Ala Trp Trp Gly Glu Ser Thr Thr  
 115 120 125

Asp Gly Val Pro Pro Ser Trp Ile Asn Asn Phe Leu Pro Thr Asp Asn  
 130 135 140

Lys Glu Asn Asp Glu Lys Phe Glu Ala Val Gly His Trp Thr Gln Met  
 145 150 155 160

Ala Trp Ala Lys Thr Tyr Gln Ile Gly Cys Ala Leu Lys Val Cys His  
 165 170 175

Lys Pro Asp Cys Asn Gly Asn Leu Ile Asp Cys Arg Tyr Tyr Pro Gly  
180 185 190

Gly Asn Gly Met Gly Ser Pro Ile Tyr Gln Gln Gly Lys Pro Ala Ser  
195 200 205

Gly Cys Gly Lys Ala Gly Pro Ser Thr Lys Tyr Ser Gly Leu Cys Lys  
210 215 220

Pro Asp Pro His Gln Asn Asn  
225 230